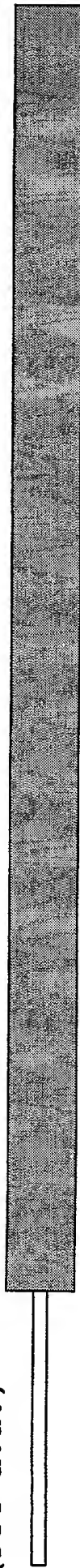


Structure of HTPL and alignment of Patched motifs.

FIG. 1A

HTPL-L (954 a.a.)



HTPL-S (767 a.a.)



Patched

FIG. 1B

Patched motif

Patched motif		10	20	30	40	50	60	70	80
consensus	********
HTPL-L		1 VLSSKIRYTFTPDDIRSYTERGSRSEHEPL-VERKFFPGDGYPISRFSIITAKARNS-NILDIRYLNEVVQVNDFISTNV	162 deeedleehyTPVGSPAKAERRFVQGHFTTnDSYRFSASRRSTEANFVSLLVVSYS-D-SLLDPATFAEVSKLDGAVQDLR	240 gi 1825729	47 NPLSDAVYLFTPLGAQSKMERMSIHEKWPL-TDNNYIPGRAVTQSREIQVTALARNDsNILDPKFANAVYQLDKYIQTRV	125 gi 1707052	22 NVVYSLLMIFGPY--SYTERRIIHDAPWL-VDGTFVAGRAVTQSREVOAVVARSGGNILDRVFSNELKLMESFIRNNI	97 gi 3892144	49 LRVDGPSYVFTPSDARWRREISVFNENWPL-DENKFLPGKSFEAKRFVNILIRAKDGSIMRDNVLHEIEILNQWIMNNI
consensus	********
HTPL-L		79 TIPVSG--ITLSFKDLCMRFFCDINCPVNQHYNQGIILRSNLHNSRIDLTYPMTTFFGTKIYLGPNFSGVKLDPN---PGN-	152	241 VAREKG--SQIQYQQVCARYALCVPPNPILYAWQVKNKTLNLS--SISFPAYNHRHPLYLTFGFGYILGGS---LGMg	313	126 RVLHNG--HYYSYKNLCLQYkNGGCPSNKHV---HILSDLHNHGFNITYPYFRFGSEGGYIGSSLGGVTVMKgeneTDI-	199	98 TVQFSN--RTWSFADLCLAGpDGRcANNdHI---QLASRLHQHGGINITYPTVRLSDKSAYIASALGGVKLAKgdngeNI-	171
gi 1825729		128 SIPTDDlkFNLTyQDLCLSY-DWVCGANEHIQ-MLLRRNDVNQILDHFPFRGGTKDTPVYLGGIFGDVQFFQn---GT-	200						

FIG. 1B

Patched motif (Continued)

```

consensus 153 .....|.....*.....|.....*.....|.....*.....|.....*.....| 240
HTPL-L 314 qllRAKAMRLLYLKTEDPEYDVQSKQWLTHLLDQFTNIKNIL-ALKkIEVVHFTSLSRqlEFEATSVTVIPVPHLAYI 392
gi 1825729 200 --LASAKAWFMIYHLKFHPEMSYISGEWELELGRMLTQYPEDP-YIS-ITYFHSQTLAD--ELKRNADTLIPRFIISIT 273
gi 1707052 172 --IVEATAWLLIYQLKFYPNEISYVSGLWEREFKNKMDYKKQAKYIS-ITYFHSQTLSD--ELNRNAERLAPKFIGAFV 246
gi 3892144 201 --LSDAKLTQLFYFLKQDKQKMWEEYSSKFSYALETFLNQVYSSD-VIT-LSFAHYQSLED--GLDENAKAFVNPVVSFF 274

consensus 227 .....|.....*.....|.....*.....|.....*.....|.....*.....| 320
HTPL-L 393 LIILFAVTSCTFRF-----DCIRNKMCAAFGVISAFLAVVSGFGLLHIGVPFVIIVANSPPFLIL----- 293
gi 1825729 274 LLIVFSTLCSLSFID-GSFSIDWVLSKPILSILGVVSAGIAILTGVGFLSLMGMPYNDIVGMPFLVL----- 340
gi 1707052 247 ILVCFSVLCISIVTIK-GSGYIDWVTKPILSVLGVSNAGMGIASAMGMLTYLEIQYNDIIAVMPFLVV----- 313
gi 3892144 275 VLAMYALVSSFTLKSSATKIDWISSKPLWAAAGMFSTVLSIIISAFGFLFILGVRYNVINTIIPFLIIgefqsfnmekn 354

consensus 294 .....|.....*.....|.....*.....|.....*.....|.....*.....| 400
HTPL-L 453 ---GVGVDDMFIMISAWHKTNLAGDIRERMSNVYSKAAVSITITITNIALYTGIMSSFRSVQCFCIYTGTTLLFCYFY 529
gi 1825729 341 ---AVGVDNMFLMVAAVVRTSRTHTVHERMGECLADAASVILITSSSTDVLSFGVGAITTIPAVQIFCVYTGVAIFFAFIY 417
gi 1707052 314 ---AVGTDNMFLMVASLKRTRDRNLKYDQRIAECEMADAASVILITALTDAISFGVGTTITIPAVQIFCIYTMCALLLTFFAY 390
gi 3892144 355 qipaIGIDDMFLMNACWDQTSKLSVPERMSKTLSSHAGVAVTITNVTDVMSFAIGCITDLPGIQFFCIYACVSVAFSYFY 434

consensus 371 QLTFFFAAIMAIAAGKYEMKGRHSLFLR---AVDAAETESP-----QRLDSRGSAK----- 416
HTPL-L 530 NITCFGAPMALDGKRE---VVCLCW---LKKADPKWPS-----FKKFCCEFPFG----- 571
gi 1825729 418 QITFFFAACALAMKHEASGRNSLFLie---AVSAEKKTSLSLst---fQRLFNLGSVpd----- 468
gi 1707052 391 QLTFFFCAILVYTRIIEEQGLHSIWLrp---AVTYSSTSPln---VKLFWLGSQPKplpscgvtvss----- 450
gi 3892144 435 QLTFFFSGAMAIMGEVEREKRHCLFFYrtfQLVDISKMNEEadsklQQIKRSASpafnlylssnssfsdsfskskt 514

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FIG. 1

FIG. 1B

Patched motif (Continued)

	490	500	510	520	530	540	550	560
consensus	475						
HTPL-L	-----SSKSHE--AEQ--AVVKFFLNICYPFLLNPKVRVCVLLVYLVYLAIAIYGCTNMKEGLDPAKL	475						
gi 1825729	-----SVPDEHgtDIH--PMSLFFRDYFGPFLTRSESKYFVFIYVLYIISIIYGCFFHVQEGDLRLNL	632						
gi 1707052	-----HSASHD--VKQp-LTSRFFGGEWYAPVLMHPVVRGIAWVFWIYLLGASYGCSRIKEGLEPVNL	528						
gi 3892144	-----tssvstmtsqtatSPASKH--LHHC-AATSFERNWYAPVLMQPWIRAIAGLWYLIYLGISYIGCTHLKEGLEPANL	522						
gi 3892144	515 ipaefawkeqqspnsslSKKSKD--REEKdRIVHFIGKIYGPFIILSNsvRIFSGLIFFVYLAIAIAMYGCYNFREGLNPGNL	592						
consensus	640						
HTPL-L	FLKDSPLVEYLRLEKHWVPYGLQVTVFVNNPPDLTNPENRDRNLNEMVDEFENTPYAMGKNSTKFWLRDYENFLYSFISE	555						
gi 1825729	ASDDSYITPYFNVENYFSDYGPVRVMIVTKKVDYWDKDVQRKLENTKIFEKNVY-VDKNLTEFWLDAVYQYLK--GNS	709						
gi 1707052	LVEDSYAIPHYRLLeKYFWKYGQVQIVINNAPDLRNHTSRDRVHAMVLDFAATSKHAIGMESVQFWLFEMER--YYQKELE	607						
gi 3892144	LVDSSYATPHYRVLeKHYWHYGASLQIVVSNPPDLRDPVERINMDKMASTFANCKVAIGDDSVQFWLREMq--VSEEIHK	600						
consensus	720						
HTPL-L	LEDEEEEFYDLEWFL-KSPGFSHWVGDLVWDN-KTDYETTIVVKFRFTTGGKDLSTWTDRTLLKTRGVAD EYPDFN	633						
gi 1825729	QDPNEKNTFMNNIPDFLSNFPNFQH-----DI-NISSSNEI ISSRGF-IQT'DVSSSAKKILLFQLRIA-EDCQIP	779						
gi 1707052	VQIID-SSFYGLLHHFL-ASKTNNPLAEDIYWGpmpDDDNNGTMVKSFRFILGMKDLVTTMDQTDATMSFREVAARWPEFN	685						
gi 3892144	IQYDN-EKFYDHAAQYI-YSDMSQPWWVDVWVG--RNNNSERI IKTFRFMIGMRDISITTKQTEATNTFREIASRFEQYN	676						
consensus	800						
HTPL-L	VTVFDEd-----AFFLDQILSIGPTTIQSIIWTLICMAVVCFLFIPNPNTVFVITVSI	686						
gi 1825729	LMVYNQA-----FIYFDQYAAILEDTVRNVLVASAAMFIVSLLLIIPYPLCSLWVTFAI	832						
gi 1707052	VTTFMPI-----WMFTDQYIIIIIPNTVQNI IIALLMIVIAVLFIPQPMCSLWVALAC	738						
gi 3892144	VTTYMPL-----WLFTDQYALVVPNTMQDIIIVAVACMLVISALLIPQPVCSFWAVTI	729						
gi 3892144	VVYHEVsfgnrkilndfissshscyaqknipklaFPFADQYLIILPATIQNVVISLlCMaVVSFLVPSLPSGfVIFVSI	824						

FIG. 1B

Patched motif (Continued)

	810	820	830	840	850	860	870	880	
*.....*.....*.....*.....*.....*.....								
consensus	687	ASIDIGVFGFLSLWGVLDLPISMITIIMSIGFSVDFAHIAHYHFRSHGSETPDERIADALEALGWPIQAAALSTILCVL	766						
HTPL-L	833	GSVIVGVTGFMAFWKVNLDISIMINLVICTGFSDFSAHISYAFV-SSSQPSVNQKSVEALYLLGYPVLLQSAISTIGVC	911						
gi 1825729	739	ASIDFGVIGYMTLWGVNLDAISMITIIMSIGFSVDYSAHIAYGYYVSRED-TAAGRKVEALSALGWPLSQGAMSTIIAVS	817						
gi 1707052	730	GSIDLGVLGFMTLWNVNLDIAISMITIIMSVGFSVDYSAHITYAYVISKES-TTSARVCDALGDLGWPPVAQGAMSTILAVS	808						
gi 3892144	825	VSINIGVFGYMTLWGVNLDAVSMISIIMSIGFAVDLSAHIIYAFVTSHG--DTKQRVIGALETTLGWPIFQGASSTIAGIS	902						
	890	900	910	920	930	940			
*.....*.....*.....*.....*.....*.....								
consensus	767	PLLFVPSYMWVVFVKTIFLVVVIGLLHGLIFLPIILSLFVT-----IRTSNAKIKKPSSI	821						
HTPL-L	912	VLAATAKAYIFRTFFKIMFLVMIFGAHGLIFIPVFLTFGRfi-----	954						
gi 1825729	818	VLADIPAYMIVTFFKTVVLSISLGLLHGLVFLPVLLSIFVRGCCiipssphGHPsAQKIEKQIRI	882						
gi 1707052	809	VLSDVPAYMIVTFFKTVFLAISIGFLHGLVFLPLMLSVFVGki-----fdIHISNISIKYCIYL	867						
gi 3892144	903	ILYTVDAYIILVFFKTIWLTLIGAIGHGLFFFIPIFLSLFPV-----EFFRIPKSSEL	954						

Structure of the HTPL gene (Chr. 10p12.1)

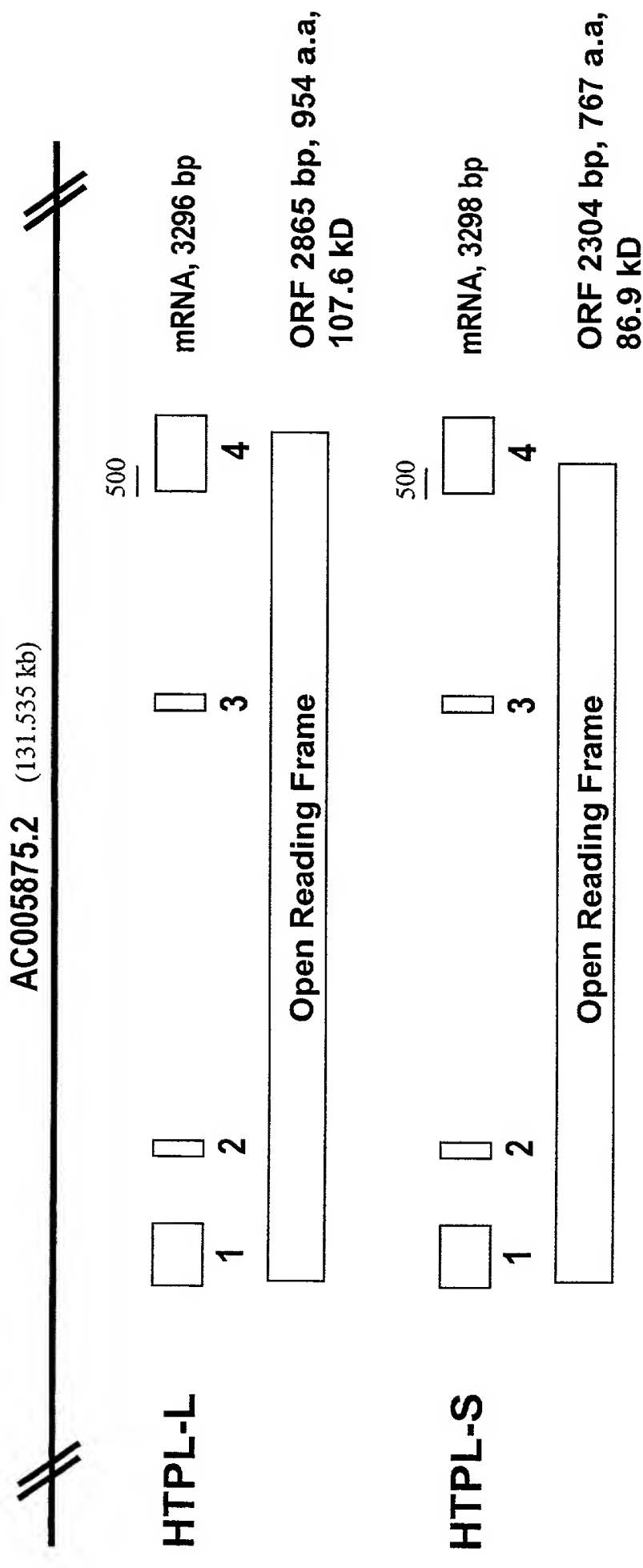


FIG. 2

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nt:  SEQ ID NO: 1
aa:  SEQ ID NO: 3
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[illegible]

FIG. 3

S	R	T	F	Q	W	L	G	W	Q	V	G	A	136
TCC	CGC	ACC	TTC	CAG	TGG	CTG	GGG	TGG	CAG	GTG	GGC	GCG	485
H	P	W	I	F	L	L	A	P	L	M	L	T	149
CAC	CCC	TGG	ATC	TTC	CTG	CTG	GCG	CCC	TTG	ATG	CTG	ACA	524
A	A	L	G	T	G	F	L	Y	L	P	K	D	162
GCC	GCG	CTG	GGC	ACC	GGC	TTC	CTG	TAC	CTA	CCC	AAG	GAC	563
E	E	E	D	L	E	E	H	Y	T	P	V	G	175
GAA	GAG	GAA	GAC	CTA	GAG	GAG	CAT	TAC	ACC	CCT	GTG	GGG	602
S	P	A	K	A	E	R	R	F	V	Q	G	H	188
AGC	CCG	GCC	AAG	GCG	GAG	CGG	CGC	TTC	GTG	CAG	GGC	CAT	641
F	T	T	N	D	S	Y	R	F	S	A	S	R	201
TTC	ACC	ACC	AAC	GAC	TCC	TAC	CGC	TTC	TCC	GCC	TCC	AGG	680
R	S	T	E	A	N	F	V	S	L	L	V	V	214
AGG	AGC	ACC	GAA	GCC	AAT	TTC	GTC	TCG	CTT	CTG	GTG	GTC	719
S	Y	S	D	S	L	L	D	P	A	T	F	A	227
TCC	TAC	AGC	GAC	TCA	CTG	CTG	GAC	CCA	GCT	ACC	TTT	GCA	758
E	V	S	K	L	D	G	A	V	Q	D	L	R	240
GAA	GTC	AGC	AAA	CTG	GAC	GGC	GCG	GTG	CAG	GAT	CTG	CGC	797
V	A	R	E	K	G	S	Q	I	Q	Y	Q	Q	253
GTG	GCG	CGG	GAA	AAG	GGA	AGC	CAG	ATC	CAG	TAC	CAG	CAG	836
V	C	A	R	Y	R	A	L	C	V	P	P	N	266
GTG	TGC	GCG	AGG	TAC	AGG	GCG	CTC	TGC	GTG	CCC	CCC	AAC	875
P	I	L	Y	A	W	Q	V	N	K	T	L	N	279
CCG	ATC	CTG	TAC	GCC	TGG	CAG	GTG	AAC	AAA	ACG	CTC	AAC	914
L	S	S	I	S	F	P	A	Y	N	H	G	R	292
CTG	AGC	AGC	ATC	TCC	TTC	CCC	GCC	TAC	AAC	CAC	GGC	AGG	953
H	P	L	Y	L	T	G	F	F	G	G	Y	I	305
CAT	CCC	CTC	TAC	CTG	ACC	GGC	TTC	TTC	GGA	GGA	TAC	ATC	992

FIG. 3

L	G	G	S	L	G	M	G	Q	L	L	L	R	318
TTG	GGG	GGC	AGC	CTA	GGA	ATG	GGC	CAG	TTA	CTC	CTG	CGG	1031
A	K	A	M	R	L	L	Y	Y	L	K	T	E	331
GCC	AAA	GCC	ATG	CGG	CTG	CTG	TAC	TAC	CTG	AAG	ACC	GAG	1070
D	P	E	Y	D	V	Q	S	K	Q	W	L	T	344
GAC	CCT	GAG	TAC	GAC	GTG	CAG	AGC	AAG	CAG	TGG	CTC	ACC	1109
H	L	L	D	Q	F	T	N	I	K	N	I	L	357
CAT	TTG	CTC	GAT	CAA	TTT	ACC	AAC	ATT	AAG	AAC	ATC	TTG	1148
A	L	K	K	I	E	V	V	H	F	T	S	L	370
GCC	TTG	AAA	AAA	ATT	GAG	GTA	GTC	CAC	TTT	ACA	TCG	CTT	1187
S	R	Q	L	E	F	E	A	T	S	V	T	V	383
TCC	AGA	CAA	CTG	GAA	TTT	GAG	GCA	ACT	TCT	GTG	ACT	GTG	1226
I	P	V	F	H	L	A	Y	I	L	I	I	L	396
ATC	CCT	GTG	TTT	CAC	CTG	GCA	TAC	ATT	CTC	ATC	ATT	CTG	1265
F	A	V	T	S	C	F	R	F	D	C	I	R	409
TTT	GCA	GTC	ACA	TCA	TGC	TTT	AGG	TTT	GAC	TGC	ATA	CGA	1304
N	K	M	C	V	A	A	F	G	V	I	S	A	422
AAC	AAA	ATG	TGT	GTT	GCG	GCC	TTT	GGA	GTG	ATT	TCT	GCT	1343
F	L	A	V	V	S	G	F	G	L	L	L	H	435
TTC	TTG	GCA	GTG	GTG	AGC	GGC	TTT	GGC	CTG	CTG	TTG	CAC	1382
I	G	V	P	F	V	I	I	V	A	N	S	P	448
ATT	GGG	GTG	CCA	TTT	GTC	ATC	ATA	GTT	GCC	AAT	TCA	CCA	1421
F	L	I	L	G	V	G	V	D	D	M	F	I	461
TTT	CTT	ATT	CTA	GGT	GTT	GGG	GTC	GAT	GAC	ATG	TTT	ATC	1460
M	I	S	A	W	H	K	T	N	L	A	G	D	474
ATG	ATT	TCT	GCC	TGG	CAT	AAG	ACC	AAC	CTT	GCA	GGT	GAC	1499
I	R	E	R	M	S	N	V	Y	S	K	A	A	487
ATA	CGA	GAG	CGG	ATG	TCC	AAT	GTC	TAT	TCA	AAA	GCG	GCA	1538

FIG. 3

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V	S	I	T	I	T	T	I	T	N	I	L	A	500
GTG	TCT	ATT	ACA	ATC	ACC	ACC	ATC	ACT	AAC	ATC	CTG	GCC	1577
L	Y	T	G	I	M	S	S	F	R	S	V	Q	513
TTA	TAT	ACA	GGG	ATT	ATG	AGC	TCT	TTT	AGG	TCC	GTA	CAA	1616
C	F	C	I	Y	T	G	T	T	L	L	F	C	526
TGT	TTT	TGC	ATC	TAT	ACA	GGA	ACG	ACC	CTG	TTA	TTT	TGC	1655
Y	F	Y	N	I	T	C	F	G	A	F	M	A	539
TAT	TTT	TAT	AAC	ATC	ACG	TGT	TTT	GGA	GCA	TTT	ATG	GCC	1694
L	D	G	K	R	E	V	V	C	L	C	W	L	552
TTG	GAT	GGT	AAA	AGA	GAA	GTA	GTC	TGC	CTA	TGC	TGG	TTG	1733
K	K	A	D	P	K	W	P	S	F	K	K	F	565
AAA	AAG	GCT	GAC	CCA	AAA	TGG	CCC	TCA	TTT	AAA	AAG	TTC	1772
C	C	F	P	F	G	S	V	P	D	E	H	G	578
TGC	TGT	TTC	CCA	TTT	GGT	TCT	GTC	CCA	GAT	GAA	CAT	GGA	1811
T	D	I	H	P	M	S	L	F	F	R	D	Y	591
ACT	GAT	ATC	CAT	CCA	ATG	AGT	TTG	TTT	TTT	AGA	GAC	TAT	1850
F	G	P	F	L	T	R	S	E	S	K	Y	F	604
TTT	GGC	CCC	TTT	CTC	ACA	AGG	AGT	GAG	TCC	AAG	TAT	TTT	1889
V	V	F	I	Y	V	L	Y	I	I	S	S	I	617
GTA	GTC	TTT	ATA	TAT	GTT	TTG	TAC	ATC	ATA	AGC	AGT	ATA	1928
Y	G	C	F	H	V	Q	E	G	L	D	L	R	630
TAT	GGG	TGT	TTC	CAT	GTG	CAG	GAA	GGT	TTA	GAC	CTT	CGA	1967
N	L	A	S	D	D	S	Y	I	T	P	Y	F	643
AAT	CTG	GCA	AGT	GAC	GAT	TCC	TAC	ATC	ACA	CCA	TAT	TTT	2006
N	V	E	E	N	Y	F	S	D	Y	G	P	R	656
AAC	GTA	GAG	GAG	AAT	TAT	TTT	TCA	GAT	TAT	GGT	CCC	AGG	2045
V	M	V	I	V	T	K	K	V	D	Y	W	D	669
GTT	ATG	GTT	ATT	GTT	ACT	AAA	AAA	GTT	GAC	TAC	TGG	GAT	2084

FIG. 3

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K	D	V	R	Q	K	L	E	N	C	T	K	I	682
AAA	GAT	GTT	AGG	CAA	AAA	CTG	GAA	AAC	TGT	ACT	AAA	ATT	2123
F	E	K	N	V	Y	V	D	K	N	L	T	E	695
TTT	GAA	AAA	AAT	GTC	TAT	GTA	GAT	AAA	AAT	CTT	ACA	GAG	2162
F	W	L	D	A	Y	V	Q	Y	L	K	G	N	708
TTT	TGG	TTA	GAT	GCA	TAT	GTG	CAA	TAT	TTA	AAA	GGT	AAC	2201
S	Q	D	P	N	E	K	N	T	F	M	N	N	721
AGC	CAA	GAT	CCT	AAT	GAG	AAG	AAT	ACT	TTT	ATG	AAC	AAT	2240
I	P	D	F	L	S	N	F	P	N	F	Q	H	734
ATT	CCT	GAT	TTT	TTA	AGC	AAT	TTT	CCA	AAT	TTT	CAG	CAT	2279
D	I	N	I	S	S	S	N	E	I	I	S	S	747
GAT	ATT	AAT	ATT	TCT	TCA	TCA	AAT	GAA	ATC	ATT	TCT	TCC	2318
R	G	F	I	Q	T	T	D	V	S	S	S	A	760
CGG	GGC	TTC	ATT	CAG	ACA	ACA	GAT	GTT	TCT	TCC	TCA	GCC	2357
K	K	K	I	L	L	F	Q	L	R	R	I	A	773
AAA	AAG	AAA	ATA	TTG	TTA	TTC	CAA	TTA	CGA	CGC	ATA	GCT	2396
E	D	C	Q	I	P	L	M	V	Y	N	Q	A	786
GAA	GAC	TGT	CAA	ATT	CCC	CTA	ATG	GTG	TAT	AAC	CAG	GCA	2435
F	I	Y	F	D	Q	Y	A	A	I	L	E	D	799
TTT	ATA	TAT	TTT	GAT	CAG	TAT	GCT	GCA	ATA	TTA	GAA	GAC	2474
T	V	R	N	V	L	V	A	S	A	A	M	F	812
ACT	GTT	AGA	AAT	GTA	TTG	GTT	GCA	TCA	GCA	GCT	ATG	TTC	2513
I	V	S	L	L	L	I	P	Y	P	L	C	S	825
ATT	GTT	TCC	TTA	TTG	TTA	ATC	CCT	TAT	CCA	TTG	TGT	TCC	2552
L	W	V	T	F	A	I	G	S	V	I	V	G	838
TTG	TGG	GTG	ACT	TTT	GCT	ATC	GGT	TCT	GTG	ATT	GTA	GGG	2591
V	T	G	F	M	A	F	W	K	V	N	L	D	851
GTA	ACG	GGT	TTC	ATG	GCA	TTC	TGG	AAA	GTC	AAT	CTT	GAT	2630

FIG. 3

S	I	S	M	I	N	L	V	I	C	T	G	F	864
TCC	ATA	TCC	ATG	ATT	AAT	CTT	GTC	ATT	TGT	ACA	GGG	TTT	2669
S	F	D	F	S	A	H	I	S	Y	A	F	V	877
TCT	TTC	GAT	TTT	TCT	GCA	CAC	ATT	TCC	TAT	GCA	TTT	GTT	2708
S	S	S	Q	P	S	V	N	Q	K	S	V	E	890
TCT	AGT	TCT	CAA	CCC	TCA	GTA	AAC	CAA	AAA	TCA	GTT	GAG	2747
A	L	Y	L	L	G	Y	P	V	L	Q	S	A	903
GCA	TTG	TAT	CTT	CTA	GGC	TAC	CCA	GTG	TTA	CAA	AGT	GCA	2786
I	S	T	I	I	G	V	C	V	L	A	A	A	916
ATT	TCA	ACA	ATA	ATA	GGG	GTG	TGT	GTT	TTA	GCT	GCA	GCG	2825
K	A	Y	I	F	R	T	F	F	K	I	M	F	929
AAA	GCA	TAC	ATC	TTC	AGA	ACA	TTT	TTT	AAG	ATT	ATG	TTT	2864
L	V	M	I	F	G	A	A	H	G	L	I	F	942
CTT	GTT	ATG	ATA	TTT	GGG	GCA	GCT	CAT	GGC	CTA	ATT	TTT	2903
I	P	V	F	L	T	F	F	G	R	F	I	*	955
ATT	CCA	GTA	TTC	TTA	ACC	TTT	TTT	GGA	AGG	TTT	ATT	TGA	2942
ATATCCACTAACAAGTCAAAGACCAATTCTAGAATTCCTGATTGCCCTATTC													2994
CAATCTGATTTTTTTTAAATGCACTATTAAGAATAGTCAACAACTACTGGGA													3046
GGCCAAAGTGGGTGGATCACCTGAGGTCAAGAATTCGAGACCAGCCTGGCCA													3098
ACATGGTGAAACCTCGACACTACTGAAAATACAAAAATTATCCAGGCATGGT													3150
GGCGTGACCTATAATCCCAGCTACCTGGGAGGCTGAGGCAGGAGAATCGCT													3202
TGAACCTGGGAGATGGAGGTTGCAGTGAGCTGGAGTGCACCAGGCACTCCAG													3254
CCTGGGTGACAAGAATGAGACTCCGTCTCAGAAAAAAAAAAAAA													3296

FIG. 3

HTPL-S

nt: SEQ ID NO: 4

aa: SEQ ID NO: 6

CAGGAAACCGTCTGGTGGGATCTCCGCAGCTGCTTTTCACCTGCTGTTCTC 52

	M	P	W	V	E	P	6
CTGCGCTTCCTAAGAGGAAGAATCA	ATG	CCG	TGG	GTG	GAG	CCC	95

K	P	R	P	G	P	E	Q	K	P	K	L	T	19
AAG	CCC	AGG	CCG	GGG	CCG	GAG	CAG	AAG	CCC	AAG	CTC	ACC	134

K	P	D	S	A	T	G	P	Q	W	Y	Q	E	32
AAA	CCG	GAC	TCT	GCC	ACC	GGG	CCG	CAG	TGG	TAC	CAG	GAA	173

S	Q	E	S	E	S	E	G	K	Q	P	P	P	45
TCT	CAG	GAA	TCG	GAG	TCG	GAA	GGC	AAG	CAG	CCA	CCC	CCG	212

G	P	L	A	P	P	K	S	P	E	P	S	G	58
GGA	CCC	CTG	GCA	CCC	CCG	AAA	TCC	CCC	GAA	CCC	TCA	GGA	251

P	L	A	S	E	Q	D	A	P	L	P	E	G	71
CCC	CTG	GCG	TCG	GAG	CAG	GAT	GCA	CCC	CTG	CCA	GAG	GGG	290

D	D	A	P	P	R	P	S	M	L	D	D	A	84
GAC	GAT	GCA	CCC	CCC	CGG	CCG	TCG	ATG	CTG	GAC	GAT	GCA	329

P	R	L	P	L	E	L	D	D	A	P	L	P	97
CCC	CGC	CTG	CCG	CTG	GAG	CTG	GAC	GAT	GCA	CCC	CTG	CCG	368

E	E	E	T	P	E	P	T	A	I	C	R	H	110
GAG	GAG	GAA	ACC	CCC	GAA	CCC	ACG	GCC	ATC	TGC	AGG	CAC	407

R	H	R	C	H	T	D	C	L	E	G	L	L	123
CGG	CAC	CGC	TGT	CAC	ACC	GAC	TGC	CTA	GAG	GGG	CTG	CTG	446

S	R	T	F	Q	W	L	G	W	Q	V	G	A	136
TCC	CGC	ACC	TTC	CAG	TGG	CTG	GGG	TGG	CAG	GTG	GGC	GCG	485

FIG. 4

H	P	W	I	F	L	L	A	P	L	M	L	T	149
CAC	CCC	TGG	ATC	TTC	CTG	CTG	GCG	CCC	TTG	ATG	CTG	ACA	524
A	A	L	G	T	G	F	L	Y	L	P	K	D	162
GCC	GCG	CTG	GGC	ACC	GGC	TTC	CTG	TAC	CTA	CCC	AAG	GAC	563
E	E	E	D	L	E	E	H	Y	T	P	V	G	175
GAA	GAG	GAA	GAC	CTA	GAG	GAG	CAT	TAC	ACC	CCT	GTG	GGG	602
S	P	A	K	A	E	R	R	F	V	Q	G	H	188
AGC	CCG	GCC	AAG	GCG	GAG	CGG	CGC	TTC	GTG	CAG	GGC	CAT	641
F	T	T	N	D	S	Y	R	F	S	A	S	R	201
TTC	ACC	ACC	AAC	GAC	TCC	TAC	CGC	TTC	TCC	GCC	TCC	AGG	680
R	S	T	E	A	N	F	V	S	L	L	V	V	214
AGG	AGC	ACC	GAA	GCC	AAT	TTC	GTC	TCG	CTT	CTG	GTG	GTC	719
S	Y	S	D	S	L	L	D	P	A	T	F	A	227
TCC	TAC	AGC	GAC	TCA	CTG	CTG	GAC	CCA	GCT	ACC	TTT	GCA	758
E	V	S	K	L	D	G	A	V	Q	D	L	R	240
GAA	GTC	AGC	AAA	CTG	GAC	GGC	GCG	GTG	CAG	GAT	CTG	CGC	797
V	A	R	E	K	G	S	Q	I	Q	Y	Q	Q	253
GTG	GCG	CGG	GAA	AAG	GGA	AGC	CAG	ATC	CAG	TAC	CAG	CAG	836
V	C	A	R	Y	R	A	L	C	V	P	P	N	266
GTG	TGC	GCG	AGG	TAC	AGG	GCG	CTC	TGC	GTG	CCC	CCC	AAC	875
P	I	L	Y	A	W	Q	V	N	K	T	L	N	279
CCG	ATC	CTG	TAC	GCC	TGG	CAG	GTG	AAC	AAA	ACG	CTC	AAC	914
L	S	S	I	S	F	P	A	Y	N	H	G	R	292
CTG	AGC	AGC	ATC	TCC	TTC	CCC	GCC	TAC	AAC	CAC	GGC	AGG	953
H	P	L	Y	L	T	G	F	F	G	G	Y	I	305
CAT	CCC	CTC	TAC	CTG	ACC	GGC	TTC	TTC	GGA	GGA	TAC	ATC	992
L	G	G	S	L	G	M	G	Q	L	L	L	R	318
TTG	GGG	GGC	AGC	CTA	GGA	ATG	GGC	CAG	TTA	CTC	CTG	CGG	1031

FIG. 4

A	K	A	M	R	L	L	Y	Y	L	K	T	E	331
GCC	AAA	GCC	ATG	CGG	CTG	CTG	TAC	TAC	CTG	AAG	ACC	GAG	1070
D	P	E	Y	D	V	Q	S	K	Q	W	L	T	344
GAC	CCT	GAG	TAC	GAC	GTG	CAG	AGC	AAG	CAG	TGG	CTC	ACC	1109
H	L	L	D	Q	F	T	N	I	K	N	I	L	357
CAT	TTG	CTC	GAT	CAA	TTT	ACC	AAC	ATT	AAG	AAC	ATC	TTG	1148
A	L	K	K	I	E	V	V	H	F	T	S	L	370
GCC	TTG	AAA	AAA	ATT	GAG	GTA	GTC	CAC	TTT	ACA	TCG	CTT	1187
S	R	Q	L	E	F	E	A	T	S	V	T	V	383
TCC	AGA	CAA	CTG	GAA	TTT	GAG	GCA	ACT	TCT	GTG	ACT	GTG	1226
I	P	V	F	H	L	A	Y	I	L	I	I	L	396
ATC	CCT	GTG	TTT	CAC	CTG	GCA	TAC	ATT	CTC	ATC	ATT	CTG	1265
F	A	V	T	S	C	F	R	F	D	C	I	R	409
TTT	GCA	GTC	ACA	TCA	TGC	TTT	AGG	TTT	GAC	TGC	ATA	CGA	1304
N	K	M	C	V	A	A	F	G	V	I	S	A	422
AAC	AAA	ATG	TGT	GTT	GCG	GCC	TTT	GGA	GTG	ATT	TCT	GCT	1343
F	L	A	V	V	S	G	F	G	L	L	L	H	435
TTC	TTG	GCA	GTG	GTG	AGC	GGC	TTT	GGC	CTG	CTG	TTG	CAC	1382
I	G	V	P	F	V	I	I	V	A	N	S	P	448
ATT	GGG	GTG	CCA	TTT	GTC	ATC	ATA	GTT	GCC	AAT	TCA	CCA	1421
F	L	I	L	G	V	G	V	D	D	M	F	I	461
TTT	CTT	ATT	CTA	GGT	GTT	GGG	GTC	GAT	GAC	ATG	TTT	ATC	1460
M	I	S	A	W	H	K	T	N	L	A	D	D	474
ATG	ATT	TCT	GCC	TGG	CAT	AAG	ACC	AAC	CTT	GCA	GAT	GAC	1499
I	R	E	R	M	S	N	V	Y	S	K	A	A	487
ATA	CGA	GAG	CGG	ATG	TCC	AAT	GTC	TAT	TCA	AAA	GCG	GCA	1538
V	S	I	T	I	T	T	I	T	N	I	L	A	500
GTG	TCT	ATT	ACA	ATC	ACC	ACC	ATC	ACT	AAC	ATC	CTG	GCC	1577

FIG. 4

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L	Y	T	G	I	M	S	S	F	R	S	V	Q	513
TTA	TAT	ACA	GGG	ATT	ATG	AGC	TCT	TTT	AGG	TCT	GTA	CAA	1616
C	F	C	I	Y	T	G	M	T	L	L	F	C	526
TGT	TTT	TGC	ATC	TAT	ACA	GGA	ATG	ACC	CTG	TTA	TTT	TGC	1655
Y	F	Y	N	I	T	C	F	G	A	F	M	A	539
TAT	TTT	TAT	AAC	ATC	ACG	TGT	TTT	GGA	GCA	TTT	ATG	GCC	1694
L	D	G	K	R	E	V	V	C	L	C	W	L	552
TTG	GAT	GGT	AAA	AGA	GAA	GTA	GTC	TGC	CTA	TGC	TGG	TTG	1733
K	K	A	D	P	K	W	P	S	F	K	K	F	565
AAA	AAG	GCT	GAC	CCA	AAA	TGG	CCC	TCA	TTT	AAA	AAG	TTC	1772
C	C	F	P	F	G	S	V	P	D	E	H	G	578
TGC	TGT	TTC	CCA	TTT	GGT	TCT	GTC	CCA	GAT	GAA	CAT	GGA	1811
T	D	I	H	P	I	S	L	F	F	R	D	Y	591
ACT	GAT	ATC	CAT	CCA	ATA	AGT	TTG	TTT	TTT	AGA	GAC	TAT	1850
F	G	P	F	L	T	R	S	E	S	K	Y	F	604
TTT	GGC	CCC	TTT	CTC	ACA	AGG	AGT	GAG	TCC	AAG	TAT	TTT	1889
V	V	F	I	Y	V	L	Y	I	I	S	S	I	617
GTA	GTC	TTT	ATA	TAT	GTT	TTG	TAC	ATC	ATA	AGC	AGT	ATA	1928
Y	G	C	F	H	V	Q	E	G	L	D	L	R	630
TAT	GGG	TGT	TTC	CAT	GTG	CAG	GAA	GGT	TTA	GAC	CTT	CGA	1967
N	L	A	S	D	D	S	Y	I	T	P	Y	F	643
AAT	CTG	GCA	AGT	GAC	GAT	TCC	TAC	ATC	ACA	CCA	TAT	TTT	2006
N	V	E	E	N	Y	F	S	D	Y	G	P	R	656
AAC	GTA	GAG	GAG	AAT	TAT	TTT	TCA	GAT	TAT	GGT	CCC	AGG	2045
V	M	V	I	V	T	K	K	V	D	Y	W	D	669
GTT	ATG	GTT	ATT	GTT	ACT	AAA	AAA	GTT	GAC	TAC	TGG	GAT	2084
K	D	V	R	Q	K	L	E	N	C	T	K	I	682
AAA	GAT	GTT	AGG	CAA	AAA	CTG	GAA	AAC	TGT	ACT	AAA	ATT	2123
F	E	K	N	V	Y	V	D	K	N	L	T	E	695
TTT	GAA	AAA	AAT	GTC	TAT	GTA	GAT	AAA	AAT	CTT	ACA	GAG	2162

FIG. 4

F	W	L	D	A	Y	V	Q	Y	L	K	G	N	708
TTT	TGG	TTA	GAT	GCA	TAT	GTG	CAA	TAT	TTA	AAA	GGT	AAC	2201
S	Q	D	P	N	E	K	N	T	F	M	N	N	721
AGC	CAA	GAT	CCT	AAT	GAG	AAG	AAT	ACT	TTT	ATG	AAC	AAT	2240
I	P	D	F	L	S	N	F	P	N	F	Q	H	734
ATT	CCT	GAT	TTT	TTA	AGC	AAT	TTT	CCA	AAT	TTT	CAG	CAT	2279
D	I	N	I	S	S	S	N	E	I	I	S	S	747
GAT	ATT	AAT	ATT	TCT	TCA	TCA	AAT	GAA	ATC	ATT	TCT	TCC	2318
R	G	F	I	Q	T	T	D	V	S	S	S	A	760
CGG	GGC	TTC	ATT	CAG	ACA	ACA	GAT	GTT	TCT	TCC	TCA	GCC	2357
K	K	K	I	L	L	F	*						768
AAA	AAG	AAA	ATA	TTG	TTA	TTC	TAA	TTACGACGCATAGCTGAAG					2400
ACTGTCAAATTCCCCTAATGGTGTATAACCAGGCATTTATATATTTTGATCA													2452
GTATGCTGCAATATTAGAAGACACTGTTAGAAATGTATTGGTTGCATCAGCA													2504
GCTATGTTCAATTGTTTCCTTATTGTTAATCCCTTATCCATTGTGTTCCTTGT													2556
GGGTGACTTTTGCTATTGGTTCTGTGATTGTAGGGGTAACGGGTTTCATGGC													2608
ATTCTGGAAAGTCAATCTTGATTCCATATCCATGATTAATCTTGTCATTTGT													2660
ATAGGGTTTTCTTTTCGATTTTTCTGTACACATTTCTATGCATTTGTTTCTA													2712
GTTCTCAACCCTCAGTAAACCAAAAATCAGTTGAGGCATTGTATCTTCTAGG													2764
CTACCCAGTGTTACAAAGTGCAATTTCAACAATAATAGGGGTGTGTGTTTTTA													2816
GCTGCAGCGAAAGCATAACATCTTCAGAACATTTTTTAAGATTATGTTTCTTG													2868
TTATGATATTTGGGGCAGCTCATGGCCTAATTTTTATTCCAGTATTCTTAAC													2920
CTTTTTTGAAGGTTTATTTGAATATCCACTAACAAGTCAAAGACCAATTCT													2972
AGAATTCCTGATTGCCCTATTCCAATCTGATTTTTTTTAAATGCACTATTAAG													3024
AATAGTCAACAACTACTGGGAGGCCAAGGTGGGTGGATCACCTGAGGTCAA													3076

FIG. 4

GAATTCGAGACCAGCCTGGCCAACATGGTGAAACCTCGACACTACTGAAAAT 3128
ACAAAAATTATCCAGGCATGGTGGCGTGCACCTATAATCCCAGCTACCTGGG 3180
AGGCTGAGGCAGGAGAATCGCTTGAACCTGGGAGATGGAGGTTGCAGTGAGC 3232
TGGAGTGCACCAGGCACTCCAGCCTGGGTGACAAGAATGAGACTCCGTCTCA 3284
GAAAAAAAAAAAAA 3298

FIG. 4

HTPL tissue distribution by RT-PCR

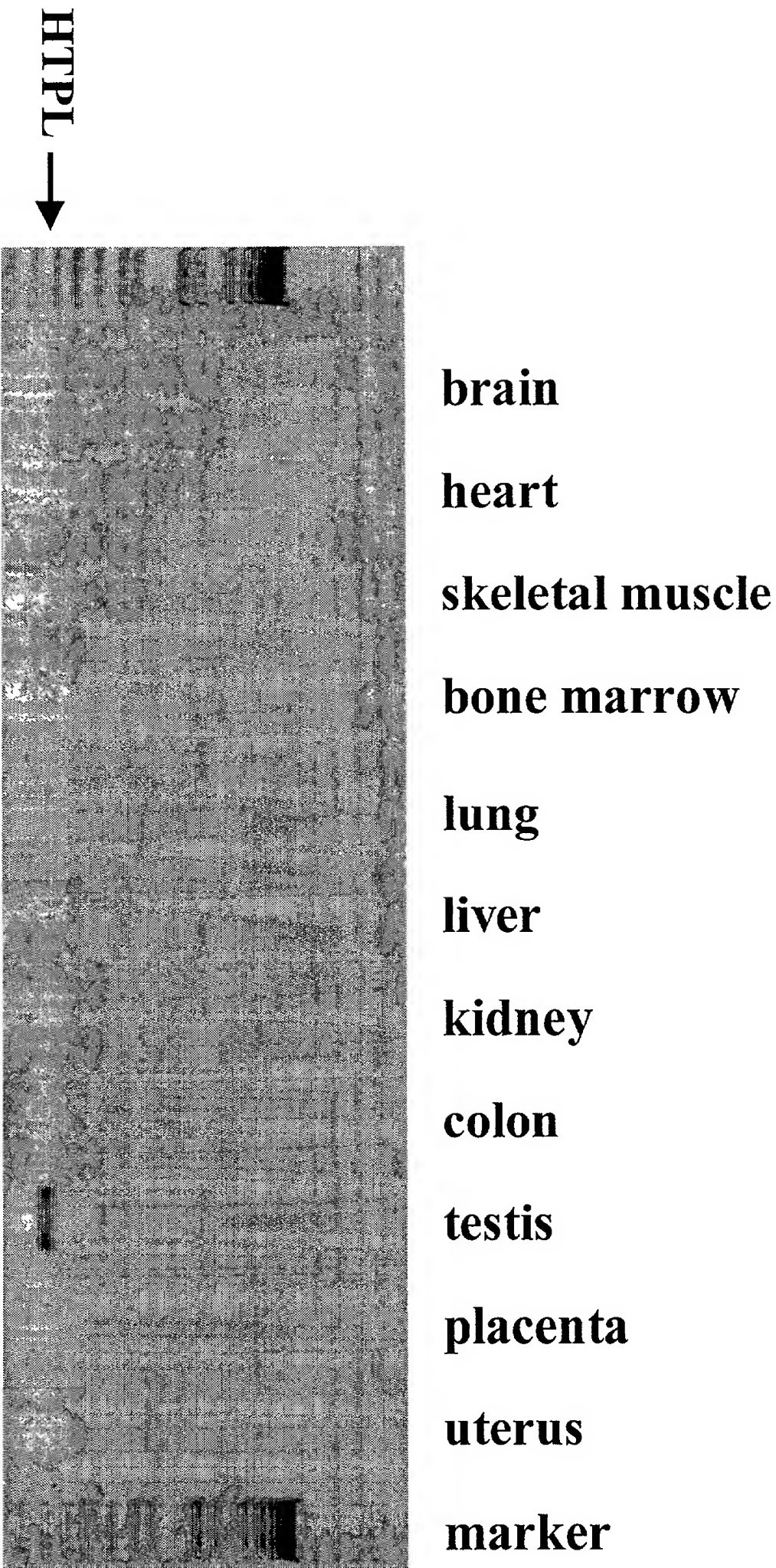


FIG. 5